```
                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:         May  4, 2005, 12:02:12 ; Search time 113.536
Seconds
                                        (without alignments)
                                        5591.830 Million cell
updates/sec

Title:          US-09-300-482-298
Perfect score:  388
Sequence:       1
ggagaaagaaagaaaagatg..........ttaaagcctgggacccccgt 388

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents_NA:*
                1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to
have a
      score greater than or equal to the score of the result being
printed,
      and is derived by analysis of the total score distribution.
```